

Supplemental Table 1. SILAC-based quantification of tryptic peptides of lamins A and C immunoprecipitated from HeLa S3 cells

Lamin A			1st experiment		2nd experiment		Averaged Ratio (Noc/DMSO)	Mean (Median)	Normalized
Start	End	Peptide sequence	Condition 1	Condition 2	Condition 1	Condition 2			Ratio
			(Light _{Noc} /Heavy _{DMSO})	(Heavy _{Noc} /Light _{DMSO})	(Light _{Noc} /Heavy _{DMSO})	(Heavy _{Noc} /Light _{DMSO})			(Noc/DMSO)
12	25	SGAQASS _T PL _S PTR	4.08	7.39	N.D.	5.86	5.77	5.40	
12	25	SGAQASSTPL _S PTR	6.36	5.40	N.D.	N.D.	5.88	5.49	
12	25	SGAQASSTPLSPTR	0.77	0.48	0.77	0.56	0.65	0.60	
29	41	LQEKEDLQELNDR	1.01	1.12	0.55	0.90	0.90	0.84	
33	41	EDLQELNDR	1.13	0.84	N.D.	0.90	0.96	0.89	
42	48	LAVYIDR	1.23	0.98	1.13	N.D.	1.11	1.04	
51	60	SLETENAGLR	1.12	1.14	1.23	0.99	1.12	1.05	
63	72	ITESEEVVSR	0.69	1.33	0.83	1.37	1.05	0.99	
79	89	AA YEAE LGDAR	1.40	1.35	1.35	1.01	1.28	1.20	
79	90	AA YEAE LGDARK	1.04	1.11	0.99	1.10	1.06	0.99	
102	108	LQLELSK	1.10	1.08	1.06	1.02	1.07	1.00	
123	133	KEGDLIAAQAR	1.18	1.08	N.D.	N.D.	1.13	1.06	
124	133	EGDLIAAQAR	1.16	0.88	1.03	1.08	1.04	0.97	
134	144	LKDLEALLNSK	0.50	0.89	0.70	1.76	0.96	0.90	
136	144	DLEALLNSK	1.09	1.03	1.17	0.93	1.05	0.98	
145	155	EAALSTALSEK	0.91	0.75	1.70	1.10	1.11	1.04	
145	156	EAALSTALSEKR	0.76	1.32	N.D.	1.07	1.05	0.98	
156	166	RTLEGELHDLR	1.15	N.D.	N.D.	N.D.	1.15	1.07	
157	166	TLEGELHDLR	0.74	1.03	1.19	0.96	0.98	0.92	
172	180	LEAALGEAK	1.08	1.05	1.00	N.D.	1.04	0.97	
172	181	LEAALGEAKK	1.12	1.12	N.D.	1.28	1.17	1.10	
181	189	KQLQDE _M LR	1.05	1.15	N.D.	1.05	1.08	1.01	
181	189	KQLQDEMLR	1.32	0.75	1.42	1.05	1.13	1.06	
182	189	QLQDE _M LR	0.93	0.97	1.04	N.D.	0.98	0.92	
182	189	QLQDEMLR	1.13	0.93	1.57	0.98	1.15	1.08	
190	196	RVDAENR	N.D.	N.D.	N.D.	0.97	0.97	0.91	
197	208	LQT _M KEELDFQK	1.02	1.07	1.05	1.03	1.04	0.97	
197	208	LQTMKEELDFQK	1.07	1.06	1.35	0.96	1.11	1.04	
202	208	EELDFQK	1.25	0.98	N.D.	0.97	1.07	1.00	
209	216	NIYSEELR	1.30	0.99	N.D.	1.04	1.11	1.04	
226	233	LVEIDNGK	1.24	1.02	N.D.	N.D.	1.13	1.05	
241	249	LADALQELR	0.98	1.30	0.66	N.D.	0.98	0.91	
250	260	AQHEDQVEQYK	1.08	1.40	1.15	1.02	1.16	1.23 (1.07)	1.08
250	261	AQHEDQVEQYKK	1.04	1.07	0.90	1.27	1.07		1.00
281	296	NSNLVGAAHEELQQSR	0.96	1.24	1.16	1.00	1.09	1.02	

297	311	IRIDSLSAQLSQLQK	1.06	1.09	1.37	N.D.	1.18	1.10
299	311	IDSLSAQLSQLQK	1.14	1.21	0.91	0.95	1.05	0.98
320	329	LRDLESLAR	1.12	0.99	1.23	0.97	1.08	1.01
322	329	DLEDSLAR	1.21	1.10	N.D.	N.D.	1.16	1.08
342	349	EREMAEMR	1.29	N.D.	N.D.	N.D.	1.29	1.20
352	366	_M QQQLDEYQELLDIK	1.03	1.11	N.D.	N.D.	1.07	1.00
352	366	MQQQLDEYQELLDIK	1.05	1.16	N.D.	N.D.	1.10	1.03
367	377	LALD _M EIHAYR	1.13	1.01	1.18	0.97	1.07	1.00
367	377	LALDMEIHAYR	1.14	1.06	N.D.	1.18	1.13	1.05
378	386	KLLEGEER	1.08	0.94	N.D.	N.D.	1.01	0.94
379	386	LLEGEER	N.D.	1.00	1.19	1.12	1.10	1.03
387	397	LRL _S P _S PTSQR	2.43	2.75	2.41	2.75	2.59	2.42
387	397	LRL _S PSPTSQR	0.41	0.49	0.49	N.D.	0.46	0.43
389	397	LSPSPTSQR	1.14	0.50	N.D.	N.D.	0.82	0.76
420	427	KLESTESR	N.D.	N.D.	1.11	0.94	1.03	0.96
428	435	SSFQHAR	N.D.	N.D.	1.48	1.01	1.24	1.16
440	450	VAVEEVDEEGK	1.07	1.04	0.93	1.68	1.18	1.10
440	453	VAVEEVDEEGKFVR	1.05	1.08	1.10	1.09	1.08	1.01
458	470	SNEDQ _S MGNWQIK	0.96	1.09	N.D.	1.11	1.06	0.99
458	470	SNEDQSMGNWQIK	1.05	1.14	1.09	1.27	1.14	1.06
471	482	RQNGDDPLLTYR	N.D.	N.D.	0.90	N.D.	0.90	0.84
472	482	QNGDDPLLTYR	1.16	0.97	N.D.	0.90	1.01	0.94
516	527	AQNTWGCNSLR	1.12	1.05	1.22	0.96	1.09	1.02
528	541	TALINSTGEEV _A _M R	1.11	N.D.	1.20	0.99	1.10	1.03
528	541	TALINSTGEEVAMR	0.54	0.83	0.95	1.05	0.84	0.79
528	542	TALINSTGEEV _A _M RK	N.D.	N.D.	N.D.	0.54	0.54	0.50
585	597	TVLCGTCGPADK	0.95	1.07	0.95	1.04	1.00	0.94
598	624	ASASGSGAQVGGPISSGSSASSVTVTR	1.07	1.04	N.D.	N.D.	1.06	0.99
628	644	SVGGSGGG _S FGDNLVTR	1.89	1.59	4.11	1.03	2.16	2.02
628	644	SVGGSGGG _S FGDNLVTR	0.68	1.05	0.82	1.03	0.89	0.84

Lamin C

			1st experiment		2nd experiment		Averaged Ratio (Noc/DMSO)	Mean (Median)	Normalized Ratio (Noc/DMSO)
Start	End	Peptide sequence	Condition 1	Condition 2	Condition 1	Condition 2			
			(Light _{Noc} /Heavy _{DMSO})	(Heavy _{Noc} /Light _{DMSO})	(Light _{Noc} /Heavy _{DMSO})	(Heavy _{Noc} /Light _{DMSO})			
12	25	SGAQASS _T PL _S PTR	N.D.	N.D.	6.91	5.49	6.20		5.49
12	25	SGAQASSTPL _S PTR	4.01	3.39	3.95	4.31	3.92		3.47
12	25	SGAQASSTPLSPTR	0.55	0.57	0.64	0.83	0.65		0.57
29	41	LQEKEDLQELNDR	1.03	N.D.	1.26	1.20	1.16		1.03
33	41	EDLQELNDR	1.17	1.07	1.08	N.D.	1.11		0.98

42	48	LAVYIDR	1.13	1.08	1.15	1.24	1.15	1.02
51	60	SLETENAGLR	0.49	1.60	0.93	1.17	1.05	0.93
63	72	ITESEEVVSR	1.00	2.46	1.34	1.42	1.56	1.38
79	89	AA YEAE LGDAR	0.92	2.02	1.29	1.41	1.41	1.25
79	90	AA YEAE LGDARK	1.00	1.22	0.99	1.29	1.13	1.00
102	108	LQLELSK	N.D.	1.16	1.00	N.D.	1.08	0.96
123	133	KEGDLIAAQAR	1.08	1.13	1.13	1.19	1.13	1.00
124	133	EGDLIAAQAR	1.09	1.06	1.23	N.D.	1.13	1.00
134	144	LKDLEALLNSK	0.40	2.53	0.67	1.05	1.16	1.03
136	144	DLEALLNSK	1.12	1.20	1.10	1.07	1.12	0.99
145	155	EAALSTALSEK	1.16	1.06	1.02	1.02	1.07	0.94
145	156	EAALSTALSEKR	1.00	1.34	1.03	1.24	1.15	1.02
157	166	TLEGELHDLR	0.56	1.54	1.08	1.52	1.17	1.04
172	180	LEAALGEAK	1.04	1.12	N.D.	N.D.	1.08	0.95
172	181	LEAALGEAKK	1.04	1.38	0.88	1.41	1.18	1.04
181	189	KQLQDE _M LR	N.D.	1.20	1.13	1.19	1.17	1.04
181	189	KQLQDEMLR	1.27	1.04	1.78	N.D.	1.37	1.21
182	189	QLQDE _M LR	0.89	1.63	N.D.	N.D.	1.26	1.11
182	189	QLQDEMLR	1.09	1.12	N.D.	1.16	1.12	0.99
197	208	LQT _M KEELDFQK	1.00	0.96	0.99	1.21	1.04	0.92
197	208	LQTMKEELDFQK	1.01	1.25	0.99	1.31	1.14	1.01
202	208	EELDFQK	1.05	1.10	1.01	N.D.	1.06	0.94
209	216	NIYSEELR	1.08	1.15	0.93	1.24	1.10	0.98
241	249	LADALQELR	0.94	1.23	0.87	1.19	1.06	0.94
250	260	AQHEDQVEQYK	1.04	1.07	1.02	1.18	1.08	0.95
250	261	AQHEDQVEQYKK	1.05	1.19	0.79	1.40	1.11	0.98
281	296	NSNLVGAAHEELQQR	0.92	1.10	0.96	1.14	1.03	0.91
297	311	IRIDSLSAQLSQLQK	1.03	1.20	N.D.	1.24	1.16	1.02
299	311	IDSLSAQLSQLQK	0.67	1.01	1.00	1.38	1.01	0.90
320	329	LRDLEDLAR	1.08	1.22	0.95	1.11	1.09	0.97
322	329	DLEDLAR	1.17	1.11	N.D.	N.D.	1.14	1.01
352	366	_M QQQLDEYQELLDIK	1.00	1.24	N.D.	N.D.	1.12	0.99
352	366	MQQQLDEYQELLDIK	1.05	1.30	N.D.	N.D.	1.18	1.04
367	377	LALD _M EIHAYR	N.D.	N.D.	1.06	N.D.	1.06	0.94
367	377	LALDMEIHAYR	1.05	1.16	N.D.	N.D.	1.11	0.98
367	378	LALDMEIHAYRK	0.86	N.D.	N.D.	N.D.	0.86	0.76
378	386	KLLEGEER	1.10	1.11	1.26	0.98	1.11	0.98
379	386	LLEGEER	N.D.	1.08	1.17	1.18	1.15	1.01
387	397	LRL _S P _S PTSQR	2.51	2.81	1.99	2.97	2.57	2.27
387	397	LRL _S PSPTSQR	0.39	0.68	N.D.	N.D.	0.53	0.47
389	397	LSPSPTSQR	0.95	0.62	N.D.	N.D.	0.79	0.70

1.27 (1.13)

402	417	ASSHSSQTQGGGSVTK	N.D.	N.D.	1.39	N.D.	1.39	1.23
420	427	KLESTESR	N.D.	N.D.	1.36	1.04	1.20	1.06
428	435	SSFSQHAR	N.D.	N.D.	0.95	N.D.	0.95	0.84
440	450	VAVEEVDEEGK	1.10	0.71	0.97	1.49	1.07	0.94
440	453	VAVEEVDEEGKFVR	1.02	1.22	1.03	1.26	1.13	1.00
458	470	SNEDQS _M GNWQIK	0.93	1.19	1.06	1.14	1.08	0.96
458	470	SNEDQSMGNWQIK	1.03	1.26	1.08	1.14	1.13	1.00
458	471	SNEDQS _M GNWQIKR	0.93	N.D.	N.D.	N.D.	0.93	0.83
471	482	RQNGDDPLLTYR	0.99	1.48	N.D.	N.D.	1.23	1.09
472	482	QNGDDPLLTYR	1.08	2.16	0.95	1.10	1.32	1.17
491	515	AGQVVTIWAAGAGATHSPPTDLVWK	1.12	N.D.	N.D.	N.D.	1.12	0.99
516	527	AQNTWGCGNSLR	1.05	1.16	1.02	1.16	1.10	0.97
528	541	TALINSTGEEVA _M R	1.14	1.19	1.07	1.11	1.13	1.00
528	541	TALINSTGEEVAMR	1.08	1.93	1.02	1.11	1.29	1.14
528	542	TALINSTGEEVA _M RK	N.D.	1.18	N.D.	N.D.	1.18	1.05

"S, T" stands for phosphorylation site and "M" stands for oxidation site.

N.D., Not detected